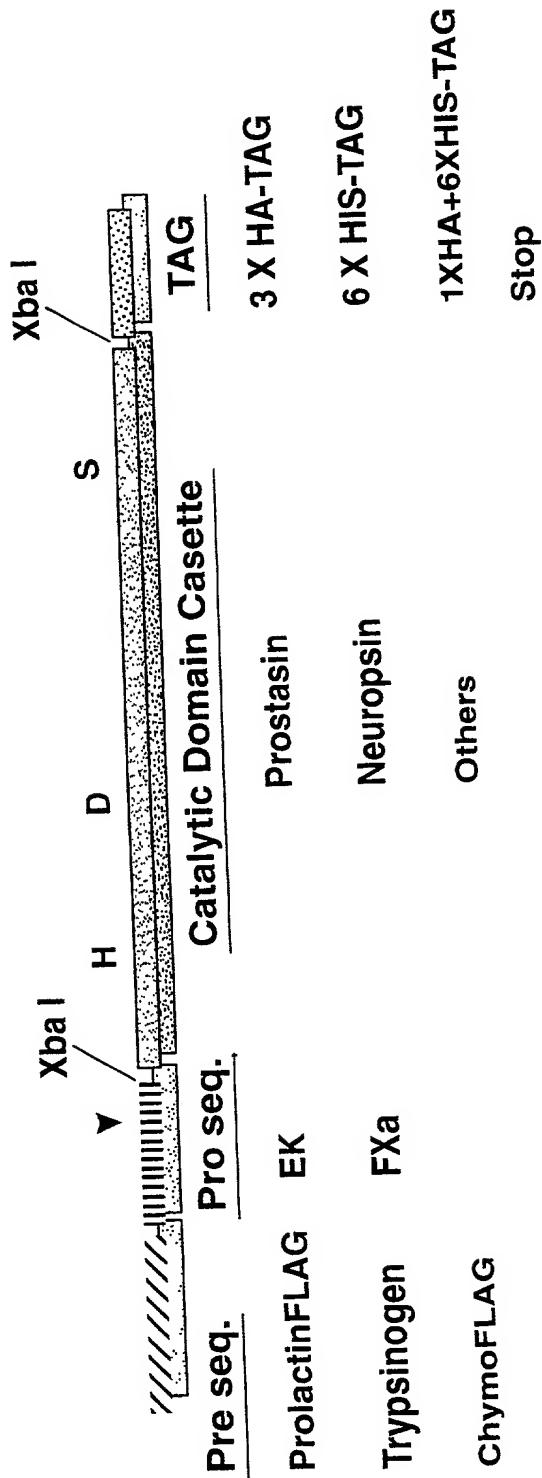


FIG. 1



SEQ. ID.NO.:1

FIG. 2(A)

Eco RI

1 GAATTCAACCACCATGGACAGCAAAGGTTCTCGCAGAAATCCGCCTGCT
 CTTAAGTGGTGGTACCTGCTTCCAAGCAGCGCTTTAGGGCGGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

50

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGTGCCAGGGTGTGGTCTCCG
 GGACGACGACCACCAAGTTAGATGAGAACACGGTCCCACACCAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

100

101 ACTACAAGGACGACGACGTGGACGCGCCGCTTGCTGCCCTTT
 TGATGTTCTGCTGCTGCACCTGCGCCGGCGAGAACGACGGGGAAA
 D Y K D D D V D A A A L A A P F
 FLAG EK2 Pro

150

151 GATGATGATGACAAGATCGTGGGGCTATGCTCTAGATAGCGGGCCGTT
 CTACTACTACTGTTCTAGCAACCCCCGATACGAGATCTATCGCCGGCGAA
 D D D D K I V G G Y A L *
 EK2 Pro

200

201 CCCTTAGTGAGGGTTAATGCTCGAGCAGACATGATAAGATAACATTGAT
 GGGAAATCACTCCAATTACGAAGCTCGTCTGTACTATTCTATGTAACTA
 SV40 Late pA

250

251 GAGTTGGACAAACCAACTAGAATGCAGTGAAAAAAATGCTTTATTTG
 CTCAAACCTGTTGGTGTGATCTACGTCACTTTTACGAAATAAAC
 SV40 Late pA

300

301 TGAAATTGTGATGCTATTGCTTATTGTAACCATTATAAGCTGCAATA
 ACTTTAACACTACGATAACGAAATAAACATTGGTAATATTGACGTTAT
 SV40 Late pA

350

351 HincII
 AACAAAGTTGAC
 TTGTTCAACTG
 361

FIG. 2(B)

SEQ. ID.NO.:2

Eco RI Not I
1 GAATTCAACCATGAATCCACTCCTGATCCTTACCTTGTGGCGGCCGCTCT 50
-----+-----+-----+-----+-----+-----+
CTTAAGTGGTACTTAGGTGAGGACTAGGAATGGAAACACCGCCGGCGAGA
M N P L L I L T F V | A A A L
Trypsinogen Pre

Xba I Not I
51 TGCTCCCCCTTGATGATGATGACAAGATCGTGGGGCTATTGTCTAG 100
-----+-----+-----+-----+-----+-----+
ACGACGGGGAAACTACTACTACTGTTCTAGCAACCCCCGATTAACAGATC
A A P F D D D D K I V G G Y C L
EK3 Pro

Not I Xba I
101 ATACCCCTACGATGTGCCGATTACGCCTAGCGGCCGCTTC 150
-----+-----+-----+-----+-----+-----+
TATGGGGATGCTACACGGGCTAATGCGGATCGCCGGGAAGGGAAATCAC
Y P Y D V P D Y A *
1 X HA-TAG

151 AGGGTTAATGCTCGAGCAGACATGATAAGATAACATTGATGAGTTGGAC 200
-----+-----+-----+-----+-----+
TCCCAATTACGAAGCTCGTCTGTACTATTCTATGTAACACTCAAACCTG
SV40 Late pA

201 AAACCACAACTAGAATGCAGTGAAAAAAATGCTTATTGTGAAATTGT 250
-----+-----+-----+-----+-----+
TTGGTGTGATCTTACGTCACTTTTACGAAATAACACTTTAAACA
SV40 Late pA

251 GATGCTATTGCTTATTGTAACCATTATAAGCTGCAATAAACAAAGTTGA 300
-----+-----+-----+-----+-----+
CTACGATAACGAAATAACATTGGTAATATTCGACGTTATTGTGTTCAACT
SV40 Late

301 C
- 301
G

FIG. 2(C)

SEQ.ID.NO.:3

Eco RI

1 GAATTCAACCACCATGGACAGCAAAGGTTCGTCGCAGAAATCCCCTGCT
 CTTAAGTGGTGGTACCTGCTGTTCCAAGCAGCGCTTTAGGGCGGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

50

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGTGCCAGGGTGTGGTCTCCG
 GGACGACGACCACACAGTTAGATGAGAACACGGTCCCACACCAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

100

101 Not I

ACTACAAGGACGACGACGTGGACGCCGCGCTTGCTGCCCTTT
 TGATGTTCTGCTGCTGCTGCACCTGCGCCGGCGAGAACGACGGGGAAA
 D Y K D D D D V D A A A L A A P F
 FLAG FXa Pro

150

151 Xba I

ATCGAGGGGCGCATTGTGGAGGGCTCGGATCTAGATACCCCTACGATGTG
 TAGCTCCCCCGCTAACACCTCCCGAGCCTAGATCTATGGGGATGCTACAC
 I E G R I V E G S D L Y P Y D V
 FXa Pro

200

201

CCCGATTACGCCGCTAGATACCCCTACGATGTGCCGATTACGCCGCTAG
 GGGCTAATGCGGCATCTATGGGGATGCTACACGGCTAAATGCGGCATC
 P D Y A A R Y P Y D V P D Y A A R
 3 X HA-TAG

250

251

ATACCACTACGATGTGCCGATTACGCCGCTAGATACCCCTACGATGTGC
 TATGGTGATGCTACACGGCTAAATGCGGCATCTATGGGGATGCTACACG
 Y H Y D V P D Y A A R Y P Y D V
 3 X HA-TAG

300

301 Not I

CCGATTACGCCCTAGCGGCCGCTTCCCTTAGTGAGGGTTAAATGCTCGAG
 GGCTAATGCGGATGCCGGCGAAGGGAAATCACTCCAAATTACGAAGCTC
 P D Y A *

350

FIG. 2(D)

351	CAGACATGATAAGATAACATTGATGAGTTGGACAAACCACA ACT TAGAATG -----+-----+-----+-----+-----+-----+ GTCTGTACTATTCTATGTAACTACTCAAACCTGTTGGTGT T GATCTTAC	400
SV40 Late pA		
401	CAGTGAAAAAAATGCTTATTTGTGAAATTGTGATGCTATT G CTTTATT -----+-----+-----+-----+-----+-----+ GTCACTTTTTTACGAAATAAACACTTTAACACACTACGATA AC GAAATAA	450
SV40 Late pA		
451	TGTAACCATTATAAGCTGCAATAAACACAGTTGAC -----+-----+-----+----- ACATTGGTAATATTGACGTTATTGTTCAACTG	484

FIG. 2(E)

SEQ. ID. NO.: 4

Eco RI

1 GAATTCAACCACCATGGACAGCAAAGGTTCGTCGCAGAAATCCGCCTGCT 50
 CTTAAGTGGTGGTACCTGTCGTTCCAAGCAGCGTCTTAGGGCGGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

51 CCTGCTGCTGGTGGTCAAATCTACTCTTGTGCCAGGGTGTGGTCTCCG 100
 GGACGACGACCACACCACAGTTAGATGAGAACACGGTCCCACACCAAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

101 Not I

ACTACAAGGACGACGACGTGGACGCGCCGCTTGCTGCCCTTT 150
 TGATGTTCCCTGCTGCTGCACCTGCGCCGGCGAGAACGACGGGGAAA
 D Y K D D D D V D A A A L A A P F
 FLAG EK1 Pro

151 Xba I

GATGATGATGACAAGATCGTTGGGGCTACAACTGTCTAGACATCACCAT 200
 CTACTACTACTGTTCTAGCAACCCCCGATGTTGACAGATCTGTAGGGTA
 D D D D K I V G G Y N C L H H H
 EK1 Pro

201 Not I

CACCATCACTAGCGGCCGCTCCCTTAGTGAGGTTAATGCTTCGAGCA 250
 GTGGTAGTGATGCCGGCGAAGGGAAATCACTCCAAATTACGAAGCTCGT
 H H H *
 6 X HIS-TAG

251

GACATGATAAGATAACATTGATGAGTTGGACAAACACAAACTAGAATGCA 300
 CTGTACTATTCTATGTAACACTCAAACCTGTTGGTGTGATCTACGT

SV40 Late pA

301

GTGAAAAAAATGCTTATTTGTGAAATTGTGATGCTATTGCTTATTTG 350
 CACTTTTTACGAAATAAACACTTAAACACTACGATAACGAATAAAC

SV40 Late pA

FIG. 2(F)

HincII

351 TAACCATTATAAGCTGCAATAAACAGTTGAC 382
 -----+-----+-----+---
 ATTGGTAATATTGACGTTATTTGTTCAACTG

FIG. 2(G)

SEQ. ID. NO.: 5

Eco RI

1 GAATTCAACCACCATGGCTTCCTCTGGCTCCTCTCCTGCTGGGCCCTCCT
 CTTAAGTGGTGGTACCGAAAGGAGACCGAGGGAGAGGACGACCCGGGAGGA
 M A F L W L L S C W A L L
 Chymotrypsinogen Pre

51 GGGTACCACCTCGGCTGGGGTCCCCGACTACAAGGACGACGACGACG
 CCCATGGTGGAAAGCCGACGCCAGGGGCTGATGTTCTGCTGCTGCTGC
 G T T F G C G V P D Y K D D D D
 Chymotrypsinogen Pre FLAG

101 Not I
 CGGCCGCTCTGCTGCCCTTGTGATGATGACAAGATCGTTGGGGC
 GCCGGCGAGAACGACGGGGAAACTACTACTACTGTCTAGCAACCCCG
 A A A L A A P F D D D D K I V G G
 EK2 Pro

151 Xba I Not I
 TATGCTCTAGACATCACCATCACCATCACTAGCGCCGCTTCCCTTAGT
 ATACGAGATCTGTAGTGGTAGTGGTAGTGTGATCGCCGGCGAAGGGAAATCA
 Y A L H H H H H H *
 6 X HIS-TAG

201 GAGGGTTAATGCTCGAGCAGACATGATAAGATACTTGTAGAGTTGGA
 CTCCCAATTACGAAGCTCGTCTGTACTATTCTATGTAACTACTCAAACCT
 SV40 Late pA

251 CAAACCACAACTAGAATGCAGTGAAAAAAATGCTTATTTGTGAAATTG
 GTTGGTGTGATCTACGTCACTTTTTACGAATAAACACTTTAAC
 SV40 Late pA

301 Hinc
 TGATGCTATTGCTTATTTGTAAACATTATAAGCTGCAATAAACAAGTTG
 ACTACGATAACGAAATAAACATTGGTAATATTCGACGTTATTGTTAAC
 SV40 Late pA

351 II
 AC
 -- 352
 TG

FIG. 2(H)

SEQ.ID.NO.:6

Eco RI
 1 GAATTCAACCACCATGGCTTCCTCTGGCTCCTCTCCTGCTGGGCCCTCCT
 CTTAAGTGGTGGTACCGAAAGGAGACCGAGGGAGAGGACGACCCGGGAGGA
 M A F L W L L S C W A L L
 Chymotrypsinogen Pre

51 GGGTACCACCTCGGCTGGGGTCCCCGACTACAAGGACGACGACGACG
 CCCATGGTGGAAAGCCGACGCCAGGGGCTGATGTTCTGCTGCTGCTGC
 G T T F G C G V P D Y K D D D D |
 Chymotrypsinogen Pre FLAG

101 Not I
 CGGCCGCTCTGCTGCCCTTGATGATGATGACAAGATCGTTGGGGC
 GCCGGCGAGAACGACGGGGAAACTACTACTACTGTTCTAGCAACCCCG
 A A A L A A P F D D D D K I V G G
 EK2 Pro

151 Xba I
 TATGCTCTAGATACCCCTACGATGTGCCGATTACGCCGCTAGACATCAC
 ATACGAGATCTATGGGATGCTACACGGGCTAATGCCGATCTGTAGTG
 Y A L | Y P Y D V P D Y A A R H H
 HA 6 X HIS-TAG

201 Not I
 CATCACCATCACTAGCGCCGCTCCCTTAGTGAGGGTTAAATGCTTCGA
 GTAGTGGTAGTGATGCCGGCGAAGGGAAATCACTCCAATTACGAAGCT
 H H H H *

251 GCAGACATGATAAGATACTTGATGAGTTGGACAAACACAACTAGAAT
 CGTCTGTACTATTCTATGTAACACTCAAACCTGTTGGTGTGATCTA
 SV40 Late pA

301 GCAGTAAAAAAATGCTTATTGTGAAATTGTGATGCTATTGCTTAT
 CGTCACCTTTTACGAAATAAACACTTAAACACTACGATAACGAAATA
 SV40 Late pA

FIG. 2(I)

HincII

351 TTGTAACCATTATAAGCTGCAATAAACAAAGTTGAC 385
 -----+-----+-----+-----+-----
 AACATTGGTAATATTGACGTTATTTGTTCAACTG

FIG. 3(A)

SEQ.ID.NO.: 7

Eco RI

1 GAATTCAACCACCATGGACAGCAAAGGTCGTCGAGAAATCCCCTGCT 50
 CTTAAGTGGTGGTACCTGCTCGTTCCAAGCAGCGTCTTAGGGCGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

51 CCTGCTGCTGGTGGTCAAATCTACTCTTGTGCCAGGGTGTGGCTCCG 100
 GGACGACGACCACACAGTTAGATGAGAACACGGTCCCACACCAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

101 Not I

ACTACAAGGACGACGACGTGGACGCGCCGCTTGCTGCCCTTT 150
 TGATGTTCCCTGCTGCTGCACCTGCGCCGGCGAGAACGACGGGGAAA
 D Y K D D D D V D A A A L A A P F
 FLAG EK2 Pro

151 Xba I

GATGATGATGACAAGATCGTTGGGGCTATGCTCTAGAGGCCGGTCAGTG 200
 CTACTACTACTGTTCTAGCAACCCCGATACGAGATCTCGGCCAGTCAC
 D D D D K I V G G Y A L E A G Q W
 EK2 Pro

201

GCCCTGGCAGGTCAAGCATCACCTATGAAGGCGTCCATGTGTGTGGCT 250
 CGGGACCGTCCAGTCGTAGTGGATACTTCCGCAGGTACACACACCACGA
 P W Q V S I T Y E G V H V C G G
 Prostasin.CDS

251

CTCTCGTGTCTGAGCAGTGGTGCTGTCAGCTGCTCACTGCTTCCCCAGC 300
 GAGAGCACAGACTCGTCACCCACGACAGTCGACGAGTGACGAAGGGTCG
 S L V S E Q W V L S A A H C F P S
 Prostasin.CDS

301

GAGCACCACAAGGAAGCCTATGAGGTCAAGCTGGGGCCACCGCTAGA 350
 CTCGTGGTGTTCCTCGGATACTCCAGTTGACCCCCGGGTGGTCGATCT
 E H H K E A Y E V K L G A H Q L D
 Prostasin.CDS

FIG. 3(B)

351 CTCCTACTCCGAGGACGCCAAGGTCAAGCACCCTGAAGGACATCATCCCC
 -----+-----+-----+-----+-----+
 GAGGATGAGGCTCCTGCGGTCCAGTCGTGGGACTTCTGTAGTAGTAGGGGG
 S Y S E D A K V S T L K D I I P H
Prostasin.CDS

401 ACCCCAGCTACCTCCAGGAGGGCTCCCAGGGCGACATTGCACTCCTCAA
 -----+-----+-----+-----+-----+
 TGGGGTCGATGGAGGTCCCTCCGAGGGTCCCGCTGTAAGTGAGGAGGT
 P S Y L Q E G S Q G D I A L L Q
Prostasin.CDS

451 CTCAGCAGACCCATCACCTTCTCCCGCTACATCCGGCCATCTGCCTCCC
 -----+-----+-----+-----+-----+
 GAGTCGTCTGGTAGTGGAGAGGGCGATGTAGGCCGGTAGACGGAGGG
 L S R P I T F S R Y I R P I C L P
Prostasin.CDS

501 TGCAGCCAACGCCCTCTTCCCCAACGGCCTCCACTGCACTGTCACTGGCT
 -----+-----+-----+-----+-----+
 ACGTCGGTTGCGGAGGAAGGGTTGCCGGAGGTGACGTGACAGTGACCGA
 A A N A S F P N G L H C T V T G
Prostasin.CDS

551 GGGGTCATGTGGCCCCCTCAGTGAGCCTCCTGACGCCAAGCCACTGCAG
 -----+-----+-----+-----+-----+
 CCCCAGTACACCGGGGGAGTCACTCGGAGGACTGCGGGTCGTGACGTC
 W G H V A P S V S L L T P K P L Q
Prostasin.CDS

601 CAACTCGAGGTGCCTCTGATCAGTCGTGAGACGTGTACTGCCTGTACAA
 -----+-----+-----+-----+-----+
 GTTGAGCTCCACGGAGACTAGTCAGCCACTCTGCACATTGACGGACATGT
 Q L E V P L I S R E T C N C L Y N
Prostasin.CDS

651 CATCGACGCCAAGCCTGAGGAGCCGCACTTGTCCAAGAGGACATGGGT
 -----+-----+-----+-----+-----+
 GTAGCTGCGGTTCGGACTCCTCGGCGTGAAACAGGTCTCCTGTACCACA
 I D A K P E E P H F V Q E D M V
Prostasin.CDS

FIG. 3(C)

701 GTGCTGGCTATGTGGAGGGGGCAAGGACGCCCTGCCAGGGT~~G~~ACTCTGGG
 -----+-----+-----+-----+-----+
 CACGACCGATACACCTCCCCCGTCTCCTGCCGACGGT~~CCC~~A~~C~~TGAGACCC
 C A G Y V E G G K D A C Q G D S G
Prostasin.CDS

751 GGCCCACCTCCTGCCCTGTGGAGGGTCTCTGGTACCTGAC~~G~~GGCATTGT
 -----+-----+-----+-----+-----+
 CGGGGTGAGAGGACGGGACACCTCCCAGAGACCATGGACT~~G~~CCC~~G~~TAACA
 G P L S C P V E G L W Y L T G I V
Prostasin.CDS

801 GAGCTGGGGAGATGCCTGTGGGGCCCGAACAGGCCTGGT~~G~~TGTACACTC
 -----+-----+-----+-----+-----+
 CTCGACCCCTCTACGGACACCCCGGGCGTTGTCCGGACCAC~~A~~CATGTGAG
 S W G D A C G A R N R P G V Y T
Prostasin.CDS

851 TGGCCTCCAGCTATGCCTCCTGGATCAAAGCAAGGTGAC~~A~~GAACCTCAG
 -----+-----+-----+-----+-----+
 ACCGGAGGTCGATA~~AC~~GGAGGACCTAGGTTCTGTTCCACTGT~~C~~TTGAGGTC
 L A S S Y A S W I Q S K V T E L Q
Prostasin.CDS

901 CCTCGTGTGGTCCCCAAACCCAGGAGTCCCAGCCGAC~~A~~GCAACCTCTG
 -----+-----+-----+-----+-----+
 GGAGCACACCACGGGTTGGGTCTCAGGGTCGGGTGT~~C~~GTTGGAGAC
 P R V V P Q T Q E S Q P D S N L C
Prostasin.CDS

951 Xba I
 TGGCAGCCACCTGGCCTTCAGCTAGACATCACCATCAC~~C~~ATCACTAGC
 -----+-----+-----+-----+-----+
 ACCGTCGGTGGACCGGAAGTCGAGATCTGTAGTGGTAGTGGT~~A~~GTGATCG
 G S H L A F S | S R | H H H H H H *
Prostasin.CDS 6 X HIS-TAG

1001 Not I
 GGCGGCTTCCCTTAGTGAGGGTAATGCTTCGAGCAGAC~~A~~TGATAAGAT
 -----+-----+-----+-----+-----+
 CGGGCGAAGGGAAATCACTCCCAATTACGAAGCTCGCTGT~~A~~CTATTCTA

FIG. 3(D)

1051 ACATTGATGAGTTGGACAAACCACAACTAGAATGCAGTGA~~AAAAA~~ATGC
 TGTAAC TACTCAAACCTGTTGGTGTGATCTTACGTCACT~~T~~TTTTTACG

1100

SV40 Late pA

1101 TTTATTGTGAAATTGTGATGCTATTGCTTATTGTAAC~~CC~~ATTATAAG
 AAATAAACACTTAAACACTACGATAACGAAATAAACATT~~G~~GTAATATT~~C~~

1150

SV40 Late pA

1151 CTGCAATAAACAAAGTTGAC
 GACGTTATTGTTCAACTG

1169

FIG. 4(A)

SEQ.ID.NO.:8

Eco RI
 1 GAATTCAACCACCATGGCTTCCTCTGGCTCCCTCCGCTGGGCCCTCCT
 CTTAAGTGGTGGTACCGAAAGGAGACCGAGGAGAGGACGACCCGGGAGGA
 M A F L W L L S C W A L L
 Chymotrypsinogen Pre

50

51 GGGTACCACCTCGGCTGGGGTCCCCGACTACAAGGACGACGACGACG
 CCCATGGTGGAAAGCCGACGCCCCAGGGCTGATGTTCTGCTGCTGCTGC
 G T T F G C G V P D Y K D D D D
 Chymotrypsinogen Pre FLAG

100

101 Not I
 CGGCCGCTCTGCTGCCCTTGATGATGATGACAAGATCGTTGGGGC
 GCCGGCGAGAACGACGGGGAAACTACTACTACTGTTCTAGCAACCCCG
 A A A L A A P F D D D D K I V G G
 EK2 Pro

150

151 Xba I
 TATGCTCTAGAGGCCGGTCAGTGGCCCTGGCAGGTACAGCATCACCTATGA
 ATACGAGATCTCCGGCCAGTCACCGGGACCGTCCAGTCGTAGTGGATACT
 Y A L E A G Q W P W Q V S I T Y E
 Prostasin.CDS

200

201 AGCGTCCATGTGTGGCTCTCGTGTCTGAGCAGTGGGTGCTGT
 TCCGCAGGTACACACACCACCGAGAGAGCACAGACTCGTCACCCACGACA
 G V H V C G G S L V S E Q W V L
 Prostasin.CDS

250

251 CAGCTGCTCACTGCTCCCCAGCGAGCACACAAGGAAGCCTATGAGGTC
 GTCGACGAGTGAAGGGGTCGCTCGTGGTGTCCCTCGGATACTCCAG
 S A A H C F P S E H H K E A Y E V
 Prostasin.CDS

300

301 AAGCTGGGGCCACCAAGCTAGACTCCTACTCCGAGGACGCCAAGGTCAG
 TTGACCCCCGGGTGGTCGATCTGAGGATGAGGCTCTGCAGGTTCCAGTC
 K L G A H Q L D S Y S E D A K V S
 Prostasin.CDS

350

FIG. 4(B)

351 CACCTGAAGGACATCATCCCCCACCCAGCTACCTCCAGGAGGGCTCCC
 -----+-----+-----+-----+-----+
 GTGGGACTTCCTGTAGTAGGGGGTGGGTCGATGGAGGTCTTCCCGAGGG
 T L K D I I P H P S Y L Q E G S
 _____ Prostasin.CDS _____

401 AGGGCGACATTGCACTCCTCCAACTCAGCAGACCCATCACCTTCTCCGC
 -----+-----+-----+-----+-----+
 TCCCGCTGTAACGTGAGGAGGTTGAGTCGTCGGTAGTGGAAAGAGGGCG
 Q G D I A L L Q L S R P I T F S R
 _____ Prostasin.CDS _____

451 TACATCCGGCCATCTGCCCTCCCTGCAGCCAACGCCCTTCCCCAACGG
 -----+-----+-----+-----+-----+
 ATGTAGGCCGGTAGACGGAGGGACGTCGGTGCAGGAAGGGTTGCC
 Y I R P I C L P A A N A S F P N G
 _____ Prostasin.CDS _____

501 CCTCCACTGCACTGTCACTGGCTGGGTCATGTGGCCCCCTCAGTGAGCC
 -----+-----+-----+-----+-----+
 GGAGGTGACGTGACAGTGACCGACCCCAGTACACCGGGGAGTCACTCGG
 L H C T V T G W G H V A P S V S
 _____ Prostasin.CDS _____

551 TCCTGACGCCAAGCCACTGCAGCAACTCGAGGTGCCTCTGATCAGTCGT
 -----+-----+-----+-----+-----+
 AGGACTGCGGGTTCGGTGACGTCGTTGAGCTCCACGGAGACTAGTCAGCA
 L L T P K P L Q Q L E V P L I S R
 _____ Prostasin.CDS _____

601 GAGACGTGTAACTGCCGTACAACATCGACGCCAAGCCTGAGGAGCCGA
 -----+-----+-----+-----+-----+
 CTCTGCACATTGACGGACATGTTGAGCTGCCACGGAGACTCCTCGGCGT
 E T C N C L Y N I D A K P E E P H
 _____ Prostasin.CDS _____

651 CTTTGTCCAAGAGGACATGGTGTGCTGGCTATGTGGAGGGGGCAAGG
 -----+-----+-----+-----+-----+
 GAAACAGGTTCTCCTGTACCAACACGACCGATAACCTCCCCCGTCC
 F V Q E D M V C A G Y V E G G K
 _____ Prostasin.CDS _____

FIG. 4(C)

701 ACGCCTGCCAGGGTGA C T G G G G C C A C T C T C C T G C C C T **G T G G A G G G T**
 -----+-----+-----+-----+-----+
 TGC GG A C G G T C C C A C T G A G A C C C C G G G T G A G A G G A C G G G A C A C C T C C A
 D A C Q G D S G G P L S C P V E G

 Prostasin.CDS

750

751 C T C T G G T A C C T G A C G G G C A T T G T G A G C T G G G G A G A T G C C T **G T G G G C C G**
 -----+-----+-----+-----+-----+
 G A G A C C A T G G A C T G C C C G T A A C A C T C G A C C C C T C T A C G G A C **A C C C G G G C**
 L W Y L T G I V S W G D A C G A R

 Prostasin.CDS

800

801 C A A C A G G C C T G G T G T G T A C A C T C T G G C C T C C A G C T A T G C C T **C C T G G A T C C**
 -----+-----+-----+-----+-----+
 G T T G T C C G G A C C A C A C A T G T G A G A C C G G A G G T C G A T A C G G A G G A C C T A G G
 N R P G V Y T L A S S Y A S W I

 Prostasin.CDS

850

851 A A A G C A A G G T G A C A G A A C T C C A G C C T C G T G G T G C C C A A A C C C A G G A G
 -----+-----+-----+-----+-----+
 T T T C G T T C C A C T G T C T T G A G G T C G G A G C A C A C C A C G G G G T T T G G G T C C T C
 Q S K V T E L Q P R V V P Q T Q E

 Prostasin.CDS

900

901 Xba I
 T C C C A G C C C G A C A G C A A C C T C T G T G G C A G C C A C C T G G C C T T **C A G C T C A G**
 -----+-----+-----+-----+-----+
 A G G G T C G G G C T G T C G T T G G A G A C A C C G T C G G T G G A C C G G A A G T C G A G A T C
 S Q P D S N L C G S H L A F S | S R

 Prostasin.CDS

950

951 Not I
 A C A T C A C C A T C A C C A T C A C T A G C G G C C G C T T C C C T T A G T **G A G G G T A A T**
 -----+-----+-----+-----+-----+
 T G T A G T G G T A G T G G T A G T G A T C G C C G G C G A A G G G A A T C A C T C C C A T T A
 | H H H H H H * |
 6 X HIS-TAG

1000

1001 G C T T C G A G C A G A C A T G A T A A G A T A C A T T G A T G A G T T G G A C A A A C C A C A A
 -----+-----+-----+-----+-----+
 C G A A G C T C G T C T G T A C T A T T C T A T G T A A C T A C T C A A A C C T G T T T G G G T T

1050

SV40 Late pA

FIG. 4(D)

1051 CTAGAATGCAGTGAAAAAAATGCTTATTTGTGAAATTGT **GATGCTATT**
 -----+-----+-----+-----+-----+-----+
 GATCTTACGTCACTTTTACGAAATAAACACTTAAAC**ACTACGATAA**

1100

SV40 Late pA

1101 GCTTATTTGTAACCATTATAAGCTGCAATAAACAGTT**GAC**
 -----+-----+-----+-----+-----+
 CGAAATAAACATTGGTAATATTCGACGTTTTGTTCAACT**TG**

1142

FIG. 5(A)

SEQ.ID.NO.:9

Eco RI

1 GAATTCAACCACCATGGACAGCAAAGGTTCGTCGCAGAAATCCCAGCTGCT 50
 CTTAAGTGGTGGTACCTGTCGTTCCAAGCAGCGTCTTAGGGCGGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGTGCCAGGGTGTGGCTCCG 100
 GGACGACGACCACACAGTTAGATGAGAACACGGTCCCACACCAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

101 ACTACAAGGACGACGACGTGGACGCCGCTCTGCTGCCCTTT 150
 TGATGTTCTGCTGCTGCACCTGCGCCGGCGAGAACGACGGGGAAA
 D Y K D D D D V D A A A L A A P F
 FLAG EK1 Pro

151 GATGATGATGACAAGATCGTGGGGCTACAACGTCTAGAAACCCATT 200
 CTACTACTACTGTTCTAGCAACCCCCGATGTTGACAGATCTTGGGTAAG
 D D D D K I V G G Y N C L E P H S
 EK1 Pro

201 GCAGCCTTGGCAGGCCCTTGTCCAGGGCCAGCAACTACTCTGGCG 250
 CGTCGGAACCGTCCGCCGAACAAGGTCCGGTCGTGATGAAGACACCGC
 Q P W Q A A L F Q G Q Q L L C G
 Neuropsin.CDS

251 GTGTCTTGTAGGTGGCAACTGGGTCTTACAGCTGCCACTGTAAAAAA 300
 CACAGGAACATCCACCGTTGACCCAGGAATGTCGACGGGTGACATTTTT
 G V L V G G N W V L T A A H C K K
 Neuropsin.CDS

301 CCGAAATACACAGTACGCCCTGGGAGACCACAGCCTACAGAAATAAAGATGG 350
 GGCTTTATGTGTCACTGCCACCCCTCTGGTGTGGATGTCTTATTTCTACC
 P K Y T V R L G D H S L Q N K D G
 Neuropsin.CDS

FIG. 5(B)

351 CCCAGAGCAAGAAATACCTGTGGTTAGTCCATCCCACACC CCTGCTACA
 -----+-----+-----+-----+-----+
 GGGTCTCGTTCTTATGGACACCAAGTCAGGTAGGGTGTGG GGACCATGT
 P E Q E I P V V Q S I P H P C Y
Neuropsin.CDS

401 ACAGCAGCGATGTGGAGGACCACAACCATGATCTGATGCTT CTTCACTG
 -----+-----+-----+-----+-----+
 TGTCGTCGCTACACCTCCTGGTGTGGTACTAGACTACGAA GAAGTTGAC
 N S S D V E D H N H D L M L L Q L
Neuropsin.CDS

451 CGTGACCAGGCATCCCTGGGTCCAAAGTGAAGCCCACAG CCTGGCAGA
 -----+-----+-----+-----+-----+
 GCACTGGTCCGTAGGGACCCAGGTTCACTTCGGTAGTC GGACCGTCT
 R D Q A S L G S K V K P I S L A D
Neuropsin.CDS

501 TCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCAGGCT GGGGACTG
 -----+-----+-----+-----+-----+
 AGTAACGTGGGTGGACCCGGTCTCACGTGGCAGACTCCGA CCCCCGTGAC
 H C T Q P G Q K C T V S G W G T
Neuropsin.CDS

551 TCACCAGTCCCCAGAGAGAATTTCTGACACTCTCACTGT GCAGAAGTA
 -----+-----+-----+-----+-----+
 AGTGGTCAGGGGCTCTCTTAAAGGACTGTGAGAGTTGACAC GTCTTCAT
 V T S P R E N F P D T L N C A E V
Neuropsin.CDS

601 AAAATCTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGG GCAGATCAC
 -----+-----+-----+-----+-----+
 TTTTAGAAAGGGTCTCTTACACTCCTACGAATGGGCC CGTCTAGTG
 K I F P Q K K C E D A Y P G Q I T
Neuropsin.CDS

651 AGATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGCTGACAC GTGCCAGG
 -----+-----+-----+-----+-----+
 TCTACCGTACCAAGACACGTCCGTGCTCGTTCCCGACTGT GCACGGTCC
 D G M V C A G S S K G A D T C Q
Neuropsin.CDS

FIG. 5(C)

701 GCGATTCTGGAGGCCCTGGTGTGATGGTGCACCCAGGGCATCACA
 CGCTAACGACCTCCGGGGGACACACACTACCACTACGTGAGGTCCCGTAGTGT
 G D S G G P L V C D G A L Q G I T
Neuropsin.CDS

751 TCCTGGGCTCAGACCCCTGTGGAGGTCCGACAAACTGGCGGTATAC
 AGGACCCCGAGTCTGGGACACCCCTCCAGGCTGTTGGACCAGATATG
 S W G S D P C G R S D K P G V Y T
Neuropsin.CDS

801 CAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCGAGG
 GTTGTAGACGGCGATGGACCTGACCTAGTTCTTAGTATCCCGTGTCC
 N I C R Y L D W I K K I I G S K
Neuropsin.CDS

851 Xba I Not I
 GCTCTAGACATCACCATCACCATCACTAGCGGCCCTCCCTTTAGGAG
 CGAGATCTGTAGTGGTAGTGGTAGTGTATCGCCGGGAAGGGAAATCACTC
 G S R H H H H H * 6 X HIS-TAG

901 GGTAAATGCTTCGAGCAGACATGATAAGATACATTGATGAGTTGGACAA
 CCAATTACGAAGCTCGTCTGTACTATTCTATGTAACACTCAAAACGTGTT
SV40 Late pA

951 ACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTGTGAAATTGTGA
 TGGTGTGATCTTACGTCACTTTTACGAAATAAACACTTTAAACACTT
SV40 Late pA

1001 TGCTATTGCTTATTGTAAACCATTATAAGCTGCAATAAACAAAGTGAC
 ACGATAACGAAATAAACATTGGTAATATTGACGTTATTGTTCACGT
SV40 Late pA

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FIG. 6(A)

SEQ. ID.NO.:10

Eco RI
1 GAATTCAACCACCATGGACAGCAAAGGTTCGTCGCAGAAATC CCGCTGCT
-----+-----+-----+-----+-----+-----+-----+
CTTAAGTGGTGGTACCTGTCGTTCCAAGCAGCGTCTTAG GGCGGACGA
M D S K G S S Q K S R I L
Prolactin Signal Sequence

50

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGTGCCAGGGT G T GGTCTCCG
-----+-----+-----+-----+-----+-----+-----+
GGACGACGACCACACAGTTAGATGAGAACACGGTCCCAC ACCAGAGGC
L L L V V S N L L L C Q G V V S
Prolactin Signal Sequence

100

101 Not I
ACTACAAGGACGACGACGTGGACGCGCCGCTTGCT GCCCCTTT
-----+-----+-----+-----+-----+-----+
TGATGTTCCCTGCTGCTGCTGCACCTGCGCCGGCGAGAACGA C GGGGGAAA
D Y K D D D D V D A A A A L A A P F
FLAG EK1 Pro

150

151 Xba I
GATGATGATGACAAGATCGTTGGGGCTACAACCTGCTAGA A AAGCACTC
-----+-----+-----+-----+-----+-----+
CTACTACTACTGTTCTAGCAACCCCCGATGTTGACAGATCT T T T C G T G A G
D D D D K I V G G Y N C L E K H S
EK1 Pro

200

201 CCAGCCCTGGCAGGCAGCCCTGTTCGAGAACGCGGCTACTCTGGGGG
-----+-----+-----+-----+-----+
GGTCGGGACCGTCCGTCGGGACAAGCTCTGCGCCGAT G A G A C A C C C
Q P W Q A A L F E K T R L L C G
Protease O.CDS

250

251 CGACGCTCATCGCCCCCAGATGGCTCCTGACAGCAGCCACTGCTCAAG
-----+-----+-----+-----+-----+
GCTGCGAGTAGCGGGGGCTACCGAGGACTGTCGTCGGGT G A C G G A G T T C
A T L I A P R W L L T A A H C L K
Protease O.CDS

300

301 CCCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAAAGGAGGG
-----+-----+-----+-----+-----+
GGGGCGATGTATCAAGTGGACCCCGTCGTGTTGGAGGTCTT CCTCCCTCCC
P R Y I V H L G Q H N L Q K E E G
Protease O.CDS

350

FIG. 6(B)

351 CTGTGAGCAGACCCGGACAGCCACTGAGTCCTTCCCCACCC **C** CGGCTCA
 -----+-----+-----+-----+-----+
 GACACTCGTCTGGGCTGTCGGTGACTCAGGAAGGGGGGGG **G** GCCGAAGT
 C E Q T R T A T E S F P H P G F
 _____ Protease O.CDS _____

401 ACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATGC **T** GGTGAAG
 -----+-----+-----+-----+-----+
 TGTTGTCGGAGGGGTTGTTCTGGTGGCGTTACTGTAGTACG **A** CCACTC
 N N S L P N K D H R N D I M L V K
 _____ Protease O.CDS _____

451 ATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCT **C** ACCCTTC
 -----+-----+-----+-----+-----+
 TACCGTAGCGGTCAAGAGGTAGTGGACCCGACACGCTGGGAG **T** GGGAGAG
 M A S P V S I T W A V R P L T L S
 _____ Protease O.CDS _____

501 CTCACGCTGTCACTGCTGGCACCAAGCTGCCTCATTCGG **C** TGGGCA
 -----+-----+-----+-----+-----+
 GAGTGCACACAGTGACGACCGTGGTCACGGAGTAAAGGC **C** GACCCGT
 S R C V T A G T S C L I S G W G
 _____ Protease O.CDS _____

551 GCACGTCCAGCCCCAGTTACGCCTGCCTCACACCTTGCAT **G** GCGAAC
 -----+-----+-----+-----+-----+
 CGTGCAGGTGGGGGTCAATGCGGACGGAGTGTGGAACGCT **A** CGGGTTG
 S T S S P Q L R L P H T L R C A N
 _____ Protease O.CDS _____

601 ATCACCATCATTGAGCACAGAAGTGTGAGAACGCCACCC **G** GCAACAT
 -----+-----+-----+-----+-----+
 TAGTGGTAGTAACCTCGTGGTCTTCACACTCTTGCAGGGG **C** CGGTGTA
 I T I I E H Q K C E N A Y P G N I
 _____ Protease O.CDS _____

651 CACAGACACCAGGTGTGCCAGCGTGCAGGAAGGGGCAAG **G** GACTCT
 -----+-----+-----+-----+-----+
 GTGTCGTGGTACACACACGGTGCACGTCTTCCCCGTT **C** CTGAGGA
 T D T M V C A S V Q E G G K D S
 _____ Protease O.CDS _____

FIG. 6(c)

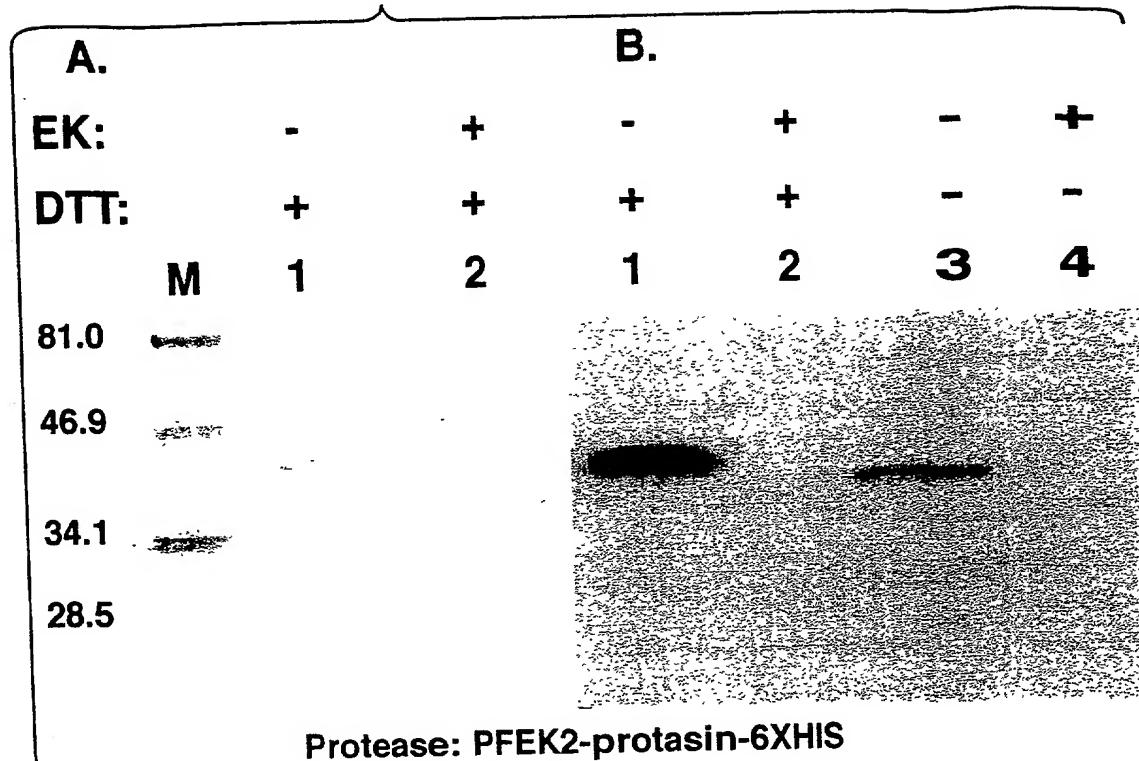
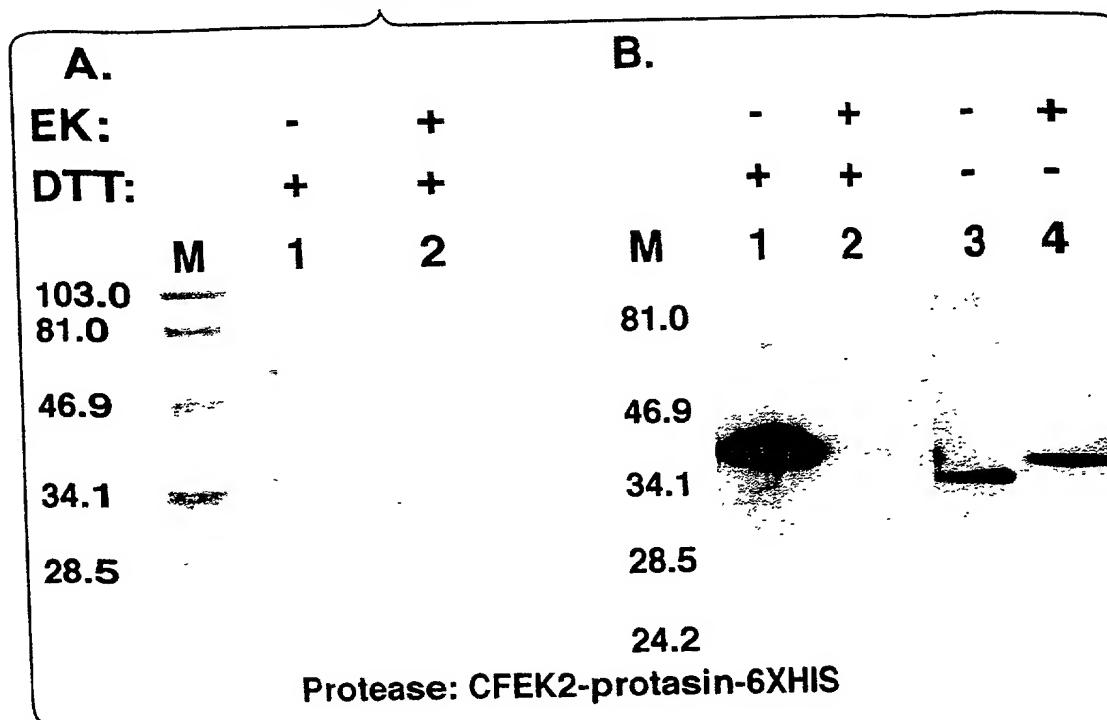
FIG. 7**FIG. 8**

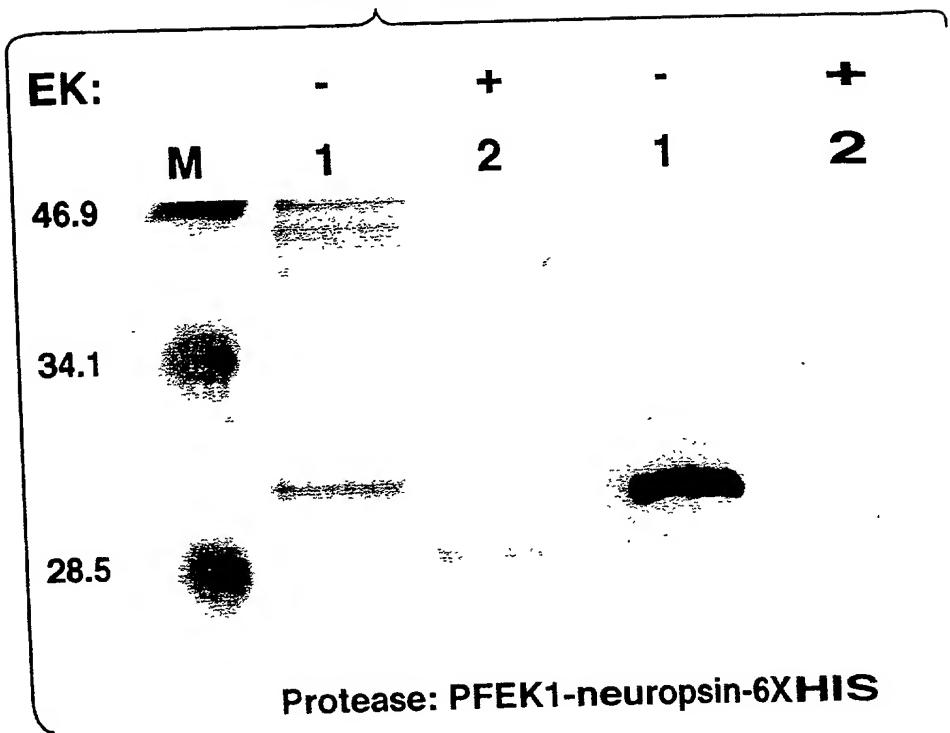
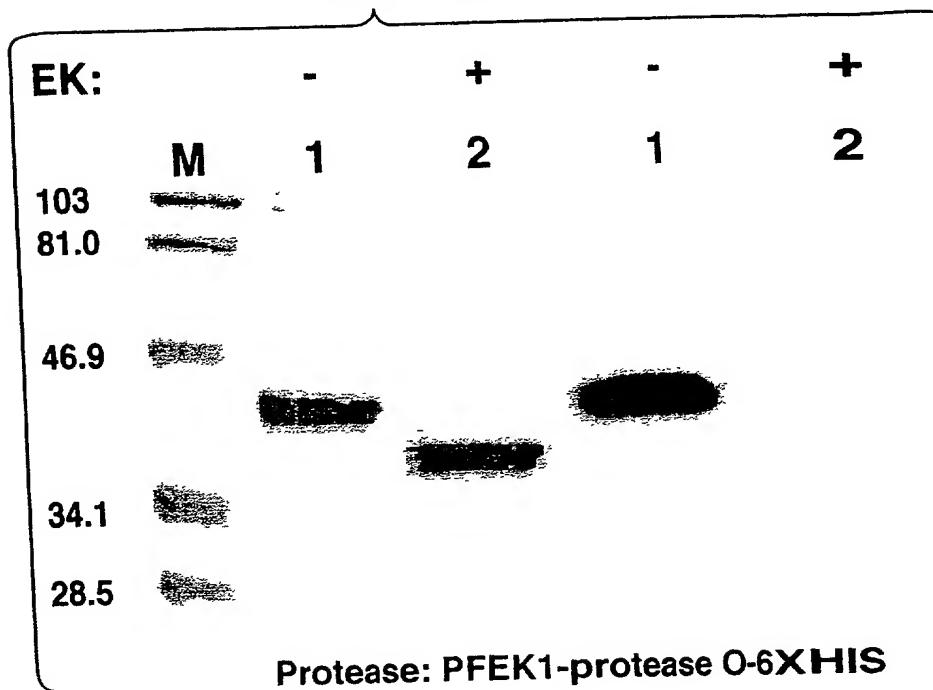
FIG. 9**FIG. 10**

FIG. 11

EK:

- + -

M 1 2 1

46.9

34.1

28.5



Protease: CFEK2-Protease F-6XHIS

FIG. 12

EK:

- + -

M 1 2 1

103

81.0

46.9

34.1

28.5



Protease: PFEK-MH2-6XHIS

FIG. 13(A)

SEQ.ID.NO.:53

Eco RI

1 GAATTCAACCACCATGGCTTCCTCTGGCTCCTCTCCTGCTG **G** GCGCTCTT
 CTTAAGTGGTGGTACCGAAAGGAGACCGAGGAGAGGACGAC **C** CGGGAGGA
 M A F L W L L S C W A I L
 Chymotrypsinogen Pre

50

51 GGGTACCACCTCGGCTGGGGTCCCCGACTACAAGGACG **A** CGACGACG
 CCCATGGTGGAAAGCCGACGCCAGGGCTGATGTTCTGC **T** GCTGCTGC
 G T T F G C G V P D Y K D D D D
 Chymotrypsinogen Pre FLAG

100

101 Not I

CGGCCGCTCTGCTGCCCTTTGATGATGATGACAAGATC **G** TTGGGGC
 GCCGGCGAGAACGACGGGGAAACTACTACTACTGTTCTAG **C** AAACCCG
 A A A L A A P F D D D D K I V G G
 EK2 Pro

150

151 Xba I

TATGCTCTAGAACTCGGGCGTTGGCCGTGGCAGGGAGCCT **T** GCGCTGTG
 ATACGAGATCTGAGCCGCAACCGCACCGTCCCTCGGA **C** CGGGACAC
 Y A L E L G R W P W Q G S L R I W
 Protease F.CDS

200

201

GGATTCCCACGTATCGGGAGTGAGCCTGCTCAGCCACCGCT **T** GGGACTCA
 CCTAAGGGTGCATACGCCCACTCGGACGAGTCGGTGGCGA **C** CCCGTGAGT
 D S H V C G V S L L S H R W A L
 Protease F.CDS

250

251

CGGCGGCGACTGCTTGAAACCTATAGTGACCTTAGTGAT **T** CCTGGGG
 GCCGCCGCGTGAACGAAACTTGGATATCACTGGAATCACT **A** GGGAGGCC
 T A A H C F E T Y S D L S D P S G
 Protease F.CDS

300

301

TGGATGGTCCAGTTGGCCAGCTGACTTCCATGCCATCCT **T** C TGGAGCCT
 ACCTACCAGGTCAAACCGGTCGACTGAAGGTACGGTAGGA **A** GACCTGGGA
 W M V Q F G Q L T S M P S F W S L
 Protease F.CDS

350

FIG. 13(B)

351 GCAGGCCTACTACAACCGTTACTCGTATCGAATATCTATCT **GAGCCCTC**
 400 CGTCGGGATGATGTTGGCAATGAAGCATAGCTTATAGATAGACTCGGGAG
 Q A Y Y N R Y F V S N I Y L S P
 Protease F.CDS

401 GCTACCTGGGAATTCACCTATGACATTGCCTTGGTGAAGCT **GTCTGCA**
 450 CGATGGACCCCTTAAGTGGGATACTGTAACGGAACCACCTCGACAGACG
 R Y L G N S P Y D I A L V K L S A
 Protease F.CDS

451 CCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAGG **CCTCAC**
 500 GGACAGTGGATGTGATTGTGTAGGTGGTAGACAGAGGTCCGGAGGTG
 P V T Y T K H I Q P I C L Q A S T
 Protease F.CDS

501 ATTTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCT **GGGGTACA**
 550 TAAACTCAAACCTTGGCCTGTCTGACGACCCACTGACCGACC **CCCATGT**
 F E F E N R T D C W V T G W G Y
 Protease F.CDS

551 TCAAAGAGGATGAGGCACTGCCATCTCCCCACACCCCTCAGG **AAAGTCAG**
 600 AGTTTCTCCTACTCCGTGACGGTAGAGGGGTGTGGGAGGTCC **TTCAGTC**
 I K E D E A L P S P H T L Q E V Q
 Protease F.CDS

601 GTCGCCATCAAACAACTCTATGTGCAACCACCTCTCCT **CAAGTACAG**
 650 CAGCGGTAGTATTGTTGAGATACACGTTGGTGGAGAAGGAGT **TTCAGTC**
 V A I I N N S M C N H L F L K Y S
 Protease F.CDS

651 TTTCCGCAAGGACATCTTGGAGACATGGTTGTGCTGGCA **ATGCCAAG**
 700 AAAGGCCTCTGTAGAACCTCTGTACCAAACACGACCGTT **ACGGGTC**
 F R K D I F G D M V C A G N A Q
 Protease F.CDS

FIG. 13(c)

701 GCGGGAAAGGATGCCTGCTTCGGTGA CTCAGGTGGACCC TTG **G** C C T G T A A C
 CGCCCTTACGGACGAAGCCACTGAGTCCACCTGGGAAC **C** G G A C A T T G
 G G K D A C F G D S G G P L A C N
 Protease F.CDS

751 AAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGG **A** G T G G G C T G
 TTCTTACCTGACACCATAGCTAACCTCAGCACTCGACCC C T C A C C C G A C
 K N G L W Y Q I G V V S W G V G C
 Protease F.CDS

801 TGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCC **A** C C A C T T G
 ACCAGCCGGGTTAGCCGGGCCACAGATGTGGTTATAGTCGG **T** G G T G A A A C
 G R P N R P G V Y T N I S H H F
 Protease F.CDS

851 A G T G G A T C C A G A A G C T G A T G G C C C A G A G T G G C A T G T C C C A G C C A G A C C C
 T C A C C T A G G T C T T C G A C T A C C G G G T C T C A C C G T A C A G G G T C G G T C T G G G G
 E W I Q K L M A Q S G M S Q P D P
 Protease F.CDS

901 Xba I Not I
 TCCTGGTCTAGACATCACCATCACCATCACTAGCGCCGCT **T** T C C C T T A G
 AGGACCAGATCTGTAGTGGTAGTGGTAGTGA T C G C C G C G A A G G G A A A T C
 S W | S R | H H H H H H *] _____
 6 X HIS-TAG

951 T G A G G G T T A A T G C T T C G A G C A G A C A T G A T A A G A T A C A T T G A T G A G T T G G
 A C T C C C A A T T A C G A A G C T C G T C T G T A C T A T T C T A T G T A A C T A C T C A A A C C
 SV40 Late pA

1001 A C A A A C C A A C T A G A A T G C A G T G A A A A A A T G C T T A T T T G T G A A A T T T
 T G T T T G G T G T G A T C T T A C G T C A C T T T T T A C G A A A T A A A C A C T T T A A A
 SV40 Late pA

1051 G T G A T G C T A T T G C T T A T T T G T A A C C A T T A A G C T G C A A T A A A C A A G G T T
 C A C T A C G A T A A C G A A A T A A A C A T T G G T A A T A T T C G A C G T T A T T T G T T C A A
 SV40 Late pA

FIG. 13(D)

1101 GAC

 CTG 1103

SEQ. ID.NO.:54

FIG. 14(A)

Eco RI
 1 GAATTCAACCACCATGGACAGCAAAGGTTCGTCGCAGAAAT C CCGCTGCT
 CTTAAGTGGTGGTACCTGTCGTTCCAAGCAGCGTCTTAGGGCGGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

50

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGTGCCAGGGT G T G G T C C G
 GGACGACGACCACACAGTTAGATGAGAACACGGTCCCACACCAGGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

100

101 Not I
 ACTACAAGGACGACGACGTGGACGCGCCGCTCTGC T G C C C C T T
 TGATGTTCCCTGCTGCTGCTGCACCTGCGCCGGCGAGAACG A C G G G G A A A
 D Y K D D D D V D A A A L A A P F
 FLAG EK1 Pro

150

151 Xba I
 GATGATGATGACAAGATCGTTGGGGCTACAACTGTCTAG A G C C G C A C T C
 CTACTACTACTGTTCTAGCAACCCCCGATGTTGACAGATC T C G G C T G A G
 D D D D K I V G G Y N C L E P H S
 EK1 Pro

200

201
 GCAGCCCTGGCAGGCGGACTGGTCATGGAAAACGAATTG T T C T G C G G
 CGTCGGGACCGTCCGCCGTGACCACTACCTTGCTTAAC A A G A C G A G C C
 Q P W Q A A L V M E N E L F C S
 MH2.CDS

250

251
 GCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGACAC T G T T C C A G
 CGCAGGACACGTAGGCGTCACCCACGACAGTCGGGTGT G A C A A G G T C
 G V L V H P Q W V L S A A H C F Q
 MH2.CDS

300

301
 AACTCCTACACCACGGGCTGGGCTGCACAGTCTTGAGG C C G A C C A A G A
 TTGAGGGATGTGGTAGCCGACCCGGACGTGTCAGAACTCC G G C T G G T C T
 N S Y T I G L G L H S L E A D Q E
 MH2.CDS

350

FIG. 14(B)

351 GCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCCAGT
 400 CGGTCCCTCGGTCTACCACCTCCGGTCGGAGAGGCATGCCGTGGGTCA
 P G S Q M V E A S L S V R H P E
 _____ MH2.CDS _____

401 ACAACAGACCCCTGCTCGCTAACGACCTCATGCTCATCAAGTTGGACGAA
 450 TGTTGTCTGGGAACGAGCGATTGCTGGAGTACGAGTAGTTCAACCTGCTT
 Y N R P L L A N D L M L I K L D E
 _____ MH2.CDS _____

451 TCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTTCCGAGTG
 500 AGGCACAGGCTCAGACTGTGGTAGGCCCTCGTAGTCGTAACGAAAGCGCAC
 S V S E S D T I R S I S I A S Q C
 _____ MH2.CDS _____

501 CCCTACCGCGGGGAACCTTGCCCTCGTTCTGGCTGGGTCTGCTGGGA
 550 GGGATGGCGCCCTTGAGAACGGAGCAAAGACCGACCCAGACGACCGCT
 P T A G N S C L V S G W G L L A
 _____ MH2.CDS _____

551 ACGGCAGAATGCCTACCGTGCTGCAGTGCCTGAAACGTGTCGGTGGTGTCT
 600 TGCGTCTTACGGATGGCACGACGTCACTGCACAGCCACCAAGAGA
 N G R M P T V L Q C V N V S V V S
 _____ MH2.CDS _____

601 GAGGAGGTCTGCAGTAAGCTCTATGACCCGCTGTACCAACCCAGCATGTT
 650 CTCCTCCAGACGTCAATTGAGATACTGGGCACATGGTGGGGTGTGACAA
 E E V C S K L Y D P L Y H P S M F
 _____ MH2.CDS _____

651 CTGCCGCCGGAGGGCACGACCAGAAGGACTCCTGCAACGGTGAACCTG
 700 GACGCCGCCCTCCGTGCTGGCTTCCTGAGGACGTTGCCACTGAGAC
 C A G G G H D Q K D S C N G D S
 _____ MH2.CDS _____

FIG. 14(C)

701 GGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTGTG **T** CTTGGA 750
 -----+-----+-----+-----+-----+
 CCCCCGGGGACTAGACGTTGCCATGAACGTCCCGAACAC **A** GAAAGCT
 G G P L I C N G Y L Q G L V S F G
 -----+-----+-----+-----+-----+
 MH2.CDS

751 AAAGCCCCGTGTGGCCAAGTTGGCGTGCAGGTGTACAC **C** AACCTCTG 800
 -----+-----+-----+-----+-----+
 TTTGGGGCACACCGGTTCAACCGCACGGTCCACAGATGTG **G** GTGGAGAC
 K A P C G Q V G V P G V Y T N L C
 -----+-----+-----+-----+-----+
 MH2.CDS

801 CAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTT **C** TAGACATC 850
 -----+-----+-----+-----+-----+
 GTTAAGTGAACCTATCTCTTGGCAGGTCCGGTCAA **A** GATCTGTAG
 K F T E W I E K T V Q A S S R H
 -----+-----+-----+-----+-----+
 MH2.CDS

851 ACCATCACCATCACTAGCGCCGCTTCCCTTACTGAGGGT **T** AATGTTC 900
 -----+-----+-----+-----+-----+
 TGGTAGTGGTAGTGAATCGCCGGCGAAGGGAAATCACTCC **A** ATACGAAG
 H H H H H *
 -----+-----+-----+-----+-----+
 6 X HIS-TAG

901 GAGCAGACATGATAAGATAACATTGATGAGTTGGACAAAC **C** AACAGA 950
 -----+-----+-----+-----+-----+
 CTCGTCTGTACTATTCTATGTAACACTCAAACCTGTTGG **T** GTGATCT
 -----+-----+-----+-----+-----+
 SV40 Late pA

951 ATGCAGTAAAAAAATGCTTATTTGTGAAATTGTGATGC **T** ATTGTT
 -----+-----+-----+-----+-----+
 TACGTCACTTTTACGAAATAAACACTTAAACACTACG **A** TAACGAAA

-----+-----+-----+-----+-----+
 SV40 Late pA

1001 ATTTGTAACCATTATAAGCTGCAATAAACAAAGTTGAC
 -----+-----+-----+-----+-----+
 TAAACATTGGTAATATTGACGTTATTGTTCAACTG

1037